



## SEQUENCE LISTING

<110> Wong, Luet  
Bell, Stephen  
Carmichael, Angus

<120> PROCESS FOR OXIDISING TERPENES

<130> HO-P02196US0 (10104571)

<140> US 09/856,339

<141> 2001-05-18

<150> PCT/GB99/03873

<151> 1999-11-19

<150> GB 9825421.2

<151> 1998-11-19

<160> 23

<170> PatentIn version 3.0

<210> 1

<211> 1242

<212> DNA

<213> Pseudomonas putida

<220>

<221> misc\_feature

<222> (1)..(1242)

<223> Coding sequence

<400> 1

acgactgaaa ccatacaaag caacgcgaat cttgcccttc tgccacccca tgtgccagag	60
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gcctgggcag ttctgcaaga atcaaacgta ccgatctgg tgtggactcg ctgcaacggc	180
ggacactgga tcgccactcg cggccaactg atccgtgagg cctatgaaga ttaccgccac	240
ttttccagcg agtgcccgtt catccctcgt gaagccggcg aagcctacga cttcattccc	300
acctcgatgg atccgcccga gcagcgccag tttcgtgctc tggccaacca agtggttggc	360
atgccggtgg tggataagct ggagaaccgg atccaggagc tggcctgctc gctgatcgag	420
agcctgcgcc cgcaaggaca gtgcaacttc accgaggact acgccgaacc cttcccgata	480
cgcattctca tgctgctcgc aggtctaccg gaagaagata tcccgcaatt gaaataccta	540
acggatcaga tgaccggtcc ggatggcagc atgaccttcg cagaggccaa ggaggcgtc	600
tacgactatc tgataccgat catcgagcaa cgcaggcaga agccgggaac cgacgctatc	660

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agcatcgttg ccaacggcca ggtcaatggg cgaccgatca ccagtgaaga agccaagagg	720
atgtgtggcc tggtactggt cggcggcctg gatacgggtg tcaatttcct cagcttcagc	780
atggagttcc tggccaaaag cccggagcat cgccaggagc tgatcgagcg tcccgagcgt	840
attccagccg cttgcgagga actactccgg cgcttctcgc tggttgccga tggccgcac	900
ctcacctccg attacgagtt tcatggcgtg caactgaaga aaggtgacca gatcctgcta	960
ccgcagatgc tgtctggcct ggatgagcgc gaaaacgcct gcccgatgca cgtcgacttc	1020
agtcgcaaaa aggtttcaca caccaccttt ggccacggca gccatctgtg ccttggccag	1080
cacctggccc gccgggaaat catcgtcacc ctcaaggaat ggctgaccag gattcctgac	1140
ttctccattg ccccggtgc ccagattcag cacaagagcg gcacgctcag cggcgtgcag	1200
gcactccctc tgggtctggga tccggcgact accaaagcgg ta	1242

<210> 2  
 <211> 3150  
 <212> DNA  
 <213> Bacillus megaterium

<220>  
 <221> misc\_feature  
 <222> (1)..(3150)  
 <223> Coding sequence

<400> 2	
atgacaatta aagaaatgcc tcagccaaaa acgtttggag agcttaaaaa tttaccgtta	60
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tttaaattcg aggcgcctgg tcgtgtaacg cgctacttat caagtcagcg tctaattaaa	180
gaagcatgcg atgaatcacg ctttgataaa aacttaagtc aagcgcttaa atttgtacgt	240
gattttgcag gagacgggtt atttacaagc tggacgcatg aaaaaaattg gaaaaaagcg	300
cataatactt tactttcaag cttcagtcag caggcaatga aaggctatca tgcgatgatg	360
gtcgatatcg ccgtgcagct tgttcaaaag tgggagcgtc taaatgcaga tgagcatatt	420
gaagtaccgg aagacatgac acgtttaacg cttgatacaa ttggtctttg cggtttaac	480
tatcgcttta acagctttta ccgagatcag cctcatccat ttattacaag tatgggtccgt	540
gcactggatg aagcaatgaa caagctgcag cgagcaaata cagacgaccc agcttatgat	600
gaaaacaagc gccagtttca agaagatatc aaggtgatga acgacctagt agataaaatt	660
attgcagatc gcaaagcaag cgggtgaacaa agcgatgatt tattaacgca tatgctaaac	720

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gacctgctc	caagctacaa	acaagtcaaa	cagcttaa	atgtcggcat	ggctctaaac	960
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gtgcttggag	gagaatatcc	tttagaaaaa	ggcgacgaac	taatggttct	gattcctcag	1080
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ccgcctgata	acgcaaagca	atgtgtcgac	tggttagacc	aagcgtctgc	tgatgaagta	1680
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cgcggtgaag	cagatgcaag	cgacgacttt	gaaggcacat	atgaagaatg	gcgtgaacat	1860
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ggtgcgtttt	caacgaacgt	cgtagcaagc	aaagaacttc	aacagccagg	cagtgcacga	2040
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ttaggtgtta	ttcctcgcaa	ctatgaagga	atagtaaacc	gtgtaacagc	aaggttcggc	2160
ctagatgcat	cacagcaaat	ccgtctggaa	gcagaagaag	aaaaattagc	tcatttgcca	2220
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atgcttgaac	tgcttgaaaa	ataccggcgc	tgtgaaatga	aattcagcga	atttatcgcc	2460

cttctgccaa gcatacgccc gcgctattac tcgatttctt catcacctcg tgtcgatgaa 2520  
 aaacaagcaa gcatcacggt cagcgttgtc tcaggagaag cgtggagcgg atatggagaa 2580  
 tataaaggaa ttgcgtcgaa ctatcttgcc gagctgcaag aaggagatac gattacgtgc 2640  
 tttatttcca caccgcagtc agaatttacg ctgccaaaag accctgaaac gccgcttatac 2700  
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 ctaaaagaac aaggacagtc acttgagagaa gcacatttat acttcggctg ccgttcacct 2820  
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 cttcataccg ctttttctcg catgccaaat cagccgaaaa catacgttca gcacgtaatg 2940  
 gaacaagacg gcaagaaatt gattgaactt cttgatcaag gagcgcaactt ctatatattgc 3000  
 ggagacggaa gccaaatggc acctgccgtt gaagcaacgc ttatgaaaag ctatgctgac 3060  
 gttcaccaag tgagtgaagc agacgctcgc ttatggctgc agcagctaga agaaaaaggc 3120  
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<220>  
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 <222> (1)..(7)  
 <223> Synthetic linker

<400> 3

Thr Asp Gly Thr Ser Ser Thr  
 1 5

<210> 4  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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 <223> Synthetic Linker

<400> 4

Thr Asp Gly Ala Ser Ser Ser  
 1 5

<210> 5  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
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<222> (1)..(17)  
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<400> 5

Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Ser Ser  
1 5 10 15

Thr

<210> 6  
<211> 21  
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<220>  
<221> DOMAIN  
<222> (1)..(21)  
<223> Synthetic Linker

<400> 6

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Gly Pro Ser Ser Thr  
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<210> 7  
<211> 4  
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<223> Synthetic Linker

<400> 7

Pro Leu Glu Leu  
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<210> 8  
<211> 7

<212> PRT  
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<223> Synthetic Linker

<400> 8

Thr Asp Gly Gly Ser Ser Ser  
1 5

<210> 9  
<211> 51  
<212> DNA  
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<221> misc\_feature  
<222> (1)..(51)  
<223> Synthetic Primer

<400> 9

gagattaaga attcataaac acatgggagt gcgtgccata tgaacgcaaa c

51

<210> 10  
<211> 36  
<212> DNA  
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<220>  
<221> variation  
<222> (1)..(36)  
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<400> 10

gaactgagta gtgccactga cggaggatcc tcatcg

36

<210> 11  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223> Synthetic Primer

<400> 11

cgatgaggat cctccgtcag tggcactact cagttc

36

<210> 12  
<211> 36  
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<213> ARTIFICIAL SEQUENCE

<220>  
<221> misc\_feature  
<222> (1)..(36)  
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<400> 12  
tcatcgggat cctcatcgat gtctaaagta gtgtat

36

<210> 13  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(52)  
<223> Synthetic desired coding sequence

<400> 13  
cccgataggc aatggtaatc atcgggagtc tagagcatcg aagctttcat cg

52

<210> 14  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(52)  
<223> Synthetic Primer

<400> 14  
cgatgaaagc ttcatgctc tagactcccg atgattacca ttgcctatcg gg

52

<210> 15  
<211> 24  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (1)..(24)  
<223> Synthetic Primer

<400> 15  
tcatcgacgc gtcgcgaact gctg 24

<210> 16  
<211> 69  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (1)..(69)  
<223> Synthetic Desired coding sequence

<400> 16  
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agagttcga 69

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> Synthetic Primer

<400> 17  
tcatcgaagc ttggctgttt t 21

<210> 18  
<211> 47  
<212> DNA  
<213> Artificial Sequence

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<221> misc\_feature  
<222> (1)..(47)  
<223> Synthetic Desired coding sequence

<400> 18  
acaatttcac acaggatcta gaccatatgt catcgaagct ttcacg 47

<210> 19  
<211> 47  
<212> DNA  
<213> Artificial Sequence





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	195						200					205			
Glu	Gln	Arg	Arg	Gln	Lys	Pro	Gly	Thr	Asp	Ala	Ile	Ser	Ile	Val	Ala
	210					215					220				
Asn	Gly	Gln	Val	Asn	Gly	Arg	Pro	Ile	Thr	Ser	Asp	Glu	Ala	Lys	Arg
225					230					235					240
Met	Cys	Gly	Leu	Leu	Leu	Val	Gly	Gly	Leu	Asp	Thr	Val	Val	Asn	Phe
			245						250					255	
Leu	Ser	Phe	Ser	Met	Glu	Phe	Leu	Ala	Lys	Ser	Pro	Glu	His	Arg	Gln
			260					265					270		
Glu	Leu	Ile	Glu	Arg	Pro	Glu	Arg	Ile	Pro	Ala	Ala	Cys	Glu	Glu	Leu
		275					280					285			
Leu	Arg	Arg	Phe	Ser	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	Thr	Ser	Asp
	290					295					300				
Tyr	Glu	Phe	His	Gly	Val	Gln	Leu	Lys	Lys	Gly	Asp	Gln	Ile	Leu	Leu
305					310					315					320
Pro	Gln	Met	Leu	Ser	Gly	Leu	Asp	Glu	Arg	Glu	Asn	Ala	Cys	Pro	Met
			325						330					335	
His	Val	Asp	Phe	Ser	Arg	Gln	Lys	Val	Ser	His	Thr	Thr	Phe	Gly	His
		340						345					350		
Gly	Ser	His	Leu	Cys	Leu	Gly	Gln	His	Leu	Ala	Arg	Arg	Glu	Ile	Ile
		355					360					365			
Val	Thr	Leu	Lys	Glu	Trp	Leu	Thr	Arg	Ile	Pro	Asp	Phe	Ser	Ile	Ala
	370					375					380				
Pro	Gly	Ala	Gln	Ile	Gln	His	Lys	Ser	Gly	Ile	Val	Ser	Gly	Val	Gln
385					390					395					400
Ala	Leu	Pro	Leu	Val	Trp	Asp	Pro	Ala	Thr	Thr	Lys	Ala	Val		
			405						410						

<210> 21  
 <211> 1049  
 <212> PRT  
 <213> Bacillus megaterium

<220>  
 <221> MUTAGEN  
 <222> (1)..(1049)  
 <223> Coding sequence

<400> 21

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Asn	Leu	Pro	Leu	Leu	Asn	Thr	Asp	Lys	Pro	Val	Gln	Ala	Leu	Met	Lys	20	25	30	
Ile	Ala	Asp	Glu	Leu	Gly	Glu	Ile	Phe	Lys	Phe	Glu	Ala	Pro	Gly	Arg	35	40	45	
Val	Thr	Arg	Tyr	Leu	Ser	Ser	Gln	Arg	Leu	Ile	Lys	Glu	Ala	Cys	Asp	50	55	60	
Glu	Ser	Arg	Phe	Asp	Lys	Asn	Leu	Ser	Gln	Ala	Leu	Lys	Phe	Val	Arg	65	70	75	80
Asp	Phe	Ala	Gly	Asp	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	85	90	95	
Trp	Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	100	105	110	
Met	Lys	Gly	Tyr	His	Ala	Met	Met	Val	Asp	Ile	Ala	Val	Gln	Leu	Val	115	120	125	
Gln	Lys	Trp	Glu	Arg	Leu	Asn	Ala	Asp	Glu	His	Ile	Glu	Val	Pro	Glu	130	135	140	
Asp	Met	Thr	Arg	Leu	Thr	Leu	Asp	Thr	Ile	Gly	Leu	Cys	Gly	Phe	Asn	145	150	155	160
Tyr	Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	165	170	175	
Ser	Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	180	185	190	
Asn	Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	195	200	205	
Asp	Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	210	215	220	
Lys	Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	225	230	235	240
Gly	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	245	250	255	
Tyr	Gln	Ile	Ile	Thr	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	260	265	270	
Leu	Leu	Ser	Phe	Ala	Leu	Tyr	Phe	Leu	Val	Lys	Asn	Pro	His	Val	Leu	275	280	285	
Gln	Lys	Ala	Ala	Glu	Glu	Ala	Ala	Arg	Val	Leu	Val	Asp	Pro	Ala	Pro	290	295	300	

Ser	Tyr	Lys	Gln	Val	Lys	Gln	Leu	Lys	Tyr	Val	Gly	Met	Val	Leu	Asn	
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Glu	Ala	Leu	Arg	Leu	Trp	Pro	Thr	Ala	Pro	Ala	Phe	Ser	Leu	Tyr	Ala	
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Lys	Glu	Asp	Thr	Val	Leu	Gly	Gly	Glu	Tyr	Pro	Leu	Glu	Lys	Gly	Asp	
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Glu	Leu	Met	Val	Leu	Ile	Pro	Gln	Leu	His	Arg	Asp	Lys	Thr	Ile	Trp	
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Gly	Asp	Asp	Val	Glu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Glu	Asn	Pro	Ser	
	370					375					380					
Ala	Ile	Pro	Gln	His	Ala	Phe	Lys	Pro	Phe	Gly	Asn	Gly	Gln	Arg	Ala	
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Cys	Ile	Gly	Gln	Gln	Phe	Ala	Leu	His	Glu	Ala	Thr	Leu	Val	Leu	Gly	
			405						410						415	
Met	Met	Leu	Lys	His	Phe	Asp	Phe	Glu	Asp	His	Thr	Asn	Tyr	Glu	Leu	
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Asp	Ile	Lys	Glu	Thr	Leu	Thr	Leu	Lys	Pro	Glu	Gly	Phe	Val	Val	Lys	
		435					440					445				
Ala	Lys	Ser	Lys	Lys	Ile	Pro	Leu	Gly	Gly	Ile	Pro	Ser	Pro	Ser	Thr	
	450					455					460					
Glu	Gln	Ser	Ala	Lys	Lys	Ala	Arg	Lys	Lys	Ala	Glu	Asn	Ala	His	Asn	
465					470					475					480	
Thr	Pro	Leu	Leu	Val	Leu	Tyr	Gly	Ser	Asn	Met	Gly	Thr	Ala	Glu	Gly	
				485					490					495		
Thr	Ala	Arg	Asp	Leu	Ala	Asp	Ile	Ala	Met	Ser	Lys	Gly	Phe	Ala	Pro	
			500					505					510			
Gln	Val	Ala	Thr	Leu	Asp	Ser	His	Ala	Gly	Asn	Leu	Pro	Arg	Glu	Gly	
		515					520					525				
Ala	Val	Leu	Ile	Val	Thr	Ala	Ser	Tyr	Asn	Gly	His	Pro	Pro	Asp	Asn	
		530				535					540					
Ala	Lys	Gln	Phe	Val	Asp	Trp	Leu	Asp	Gln	Ala	Ser	Ala	Asp	Glu	Val	
545					550					555					560	
Lys	Gly	Val	Arg	Tyr	Ser	Val	Phe	Gly	Cys	Gly	Asp	Lys	Asn	Trp	Ala	
				565					570					575		
Thr	Thr	Tyr	Gln	Lys	Val	Pro	Ala	Phe	Ile	Asp	Glu	Thr	Leu	Ala	Ala	
			580					585					590			
Lys	Gly	Ala	Glu	Asn	Ile	Ala	Asp	Arg	Gly	Glu	Ala	Asp	Ala	Ser	Asp	
		595					600					605				

Asp	Phe	Glu	Gly	Thr	Tyr	Glu	Glu	Trp	Arg	Glu	His	Met	Trp	Ser	Asp		
610						615					620						
Val	Ala	Ala	Tyr	Phe	Asn	Leu	Asp	Ile	Glu	Asn	Ser	Glu	Asp	Asn	Lys		
625					630					635					640		
Ser	Thr	Leu	Ser	Leu	Gln	Phe	Val	Asp	Ser	Ala	Ala	Asp	Met	Pro	Leu		
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Ala	Lys	Met	His	Gly	Ala	Phe	Ser	Thr	Asn	Val	Val	Ala	Ser	Lys	Glu		
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Leu	Gln	Gln	Pro	Gly	Ser	Ala	Arg	Ser	Thr	Arg	His	Leu	Glu	Ile	Glu		
		675					680					685					
Leu	Pro	Lys	Glu	Ala	Ser	Tyr	Gln	Glu	Gly	Asp	His	Leu	Gly	Val	Ile		
	690					695					700						
Pro	Arg	Asn	Tyr	Glu	Gly	Ile	Val	Asn	Arg	Val	Thr	Ala	Arg	Phe	Gly		
705					710					715					720		
Leu	Asp	Ala	Ser	Gln	Gln	Ile	Arg	Leu	Glu	Ala	Glu	Glu	Glu	Lys	Leu		
				725					730					735			
Ala	His	Leu	Pro	Leu	Ala	Lys	Thr	Val	Ser	Val	Glu	Glu	Leu	Leu	Gln		
			740					745					750				
Tyr	Val	Glu	Leu	Gln	Asp	Pro	Val	Thr	Arg	Thr	Gln	Leu	Arg	Ala	Met		
		755					760					765					
Ala	Ala	Lys	Thr	Val	Cys	Pro	Pro	His	Lys	Val	Glu	Leu	Glu	Ala	Leu		
	770					775					780						
Leu	Glu	Lys	Gln	Ala	Tyr	Lys	Glu	Gln	Val	Leu	Ala	Lys	Arg	Leu	Thr		
785					790					795					800		
Met	Leu	Glu	Leu	Leu	Glu	Lys	Tyr	Pro	Ala	Cys	Glu	Met	Lys	Phe	Ser		
				805					810					815			
Glu	Phe	Ile	Ala	Leu	Leu	Pro	Ser	Ile	Arg	Pro	Arg	Tyr	Tyr	Ser	Ile		
			820					825					830				
Ser	Ser	Ser	Pro	Arg	Val	Asp	Glu	Lys	Gln	Ala	Ser	Ile	Thr	Val	Ser		
		835					840					845					
Val	Val	Ser	Gly	Glu	Ala	Trp	Ser	Gly	Tyr	Gly	Glu	Tyr	Lys	Gly	Ile		
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Ala	Ser	Asn	Tyr	Leu	Ala	Glu	Leu	Gln	Glu	Gly	Asp	Thr	Ile	Thr	Cys		
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Phe	Ile	Ser	Thr	Pro	Gln	Ser	Glu	Phe	Thr	Leu	Pro	Lys	Asp	Pro	Glu		
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Thr	Pro	Leu	Ile	Met	Val	Gly	Pro	Gly	Thr	Gly	Val	Ala	Pro	Phe	Arg		
			900					905					910				

Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu  
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 Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr  
           930                          935                          940  
 Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr  
   945                          950                          955                          960  
 Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val  
                           965                          970                          975  
 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp  
                           980                          985                          990  
 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro  
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 Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val  
           1010                          1015                          1020  
 Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly  
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